



1600

RAW SEQUENCE LISTING

DATE: 08/23/2004

PATENT APPLICATION: US/09/454,223B

TIME: 10:39:22

Input Set : N:\Crf4\08202004\I454223.raw

Output Set: N:\CRF4\08232004\I454223B.raw

1 <110> APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 2 KORNBLUTH, Richard S.
 3 <120> TITLE OF INVENTION: MULTIMERIC FUSION PROTEINS OF TNF SUPERFAMILY LIGANDS
 (AMENDED)
 4 <130> FILE REFERENCE: UCSD1590
 5 <140> CURRENT APPLICATION NUMBER: US/09/454,223B
 6 <141> CURRENT FILING DATE: 1999-12-09
 7 <150> PRIOR APPLICATION NUMBER: US 60/111,471
 8 <151> PRIOR FILING DATE: 1998-12-09
 9 <160> NUMBER OF SEQ ID NOS: 22
 10 <170> SOFTWARE: PatentIn version 3.1
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 1552
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Artificial Sequence
 16 <220> FEATURE:
 17 <223> OTHER INFORMATION: Murine surfactant protein D (without the CRD) fused to the
 18 extracellular portion of human CD40L
 19 <220> FEATURE:
 20 <221> NAME/KEY: 5'UTR
 21 <222> LOCATION: (7)..(31)
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (32)..(1444)
 25 <220> FEATURE:
 26 <221> NAME/KEY: sig_peptide
 27 <222> LOCATION: (32)..(88)
 28 <223> OTHER INFORMATION: Signal peptide from murine surfactant protein D
 29 <220> FEATURE:
 30 <221> NAME/KEY: misc_feature
 31 <222> LOCATION: (88)..(799)
 32 <223> OTHER INFORMATION: Mature murine surfactant protein D including hub region,
 33 collagenous portion, and neck, but excluding carbohydrate
 34 recognition domain (CRD)
 35 <220> FEATURE:
 36 <221> NAME/KEY: misc_feature
 37 <222> LOCATION: (801)..(1546)
 38 <223> OTHER INFORMATION: Human CD40 ligand extracellular region, including stalk.
 39 <300> PUBLICATION INFORMATION:
 40 <301> AUTHORS: Motwani M
 41 <302> TITLE: Mouse surfactant protein-D. cDNA cloning, characterization, and
 42 gene localization to chromosome 14.
 43 <303> JOURNAL: J. Immunol.
 44 <304> VOLUME: 155



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45 <305> ISSUE: 12
46 <306> PAGES: 5671 TO 5677
47 <307> DATE: 1995
48 <313> RELEVANT RESIDUES: (32)..(802)
49 <300> PUBLICATION INFORMATION:
50 <301> AUTHORs: Spriggs MK
51 <302> TITLE: Recombinant human CD40 ligand stimulates B cell proliferation and
52 immunoglobulin E secretion
53 <303> JOURNAL: Journal of Experimental Medicine
54 <304> VOLUME: 176
55 <305> ISSUE: 6
56 <306> PAGES: 1543-1550
57 <307> DATE: 1992
58 <313> RELEVANT RESIDUES: (803)..(1552)
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62 1 5
63 ctt gtc ttg ctt gta cag ccc ctg gga aat ctg gga gca gaa atg aag 100
64 Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys
65 10 15 20
66 agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt 148
67 Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
68 25 30 35
69 agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga 196
70 Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
71 40 45 50 55
72 gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg 244
73 Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
74 60 65 70
75 ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga 292
76 Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
77 75 80 85
78 gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta 340
79 Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
80 90 95 100
81 agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa 388
82 Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
83 105 110 115
84 ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt 436
85 Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
86 120 125 130 135
87 cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg 484
88 Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
89 140 145 150
90 caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga 532
91 Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
92 155 160 165
93 ggt gcc cct ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga 580

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94	Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly	
95	170 175 180	
96	cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc	628
97	Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro	
98	185 190 195	
99	cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa	676
100	Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys	
101	200 205 210 215	
102	ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag	724
103	Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu	
104	220 225 230	
105	gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat	772
106	Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr	
107	235 240 245	
108	cag aaa gct gca ttg ttc cct gat ggc cat aga agg ttg gac aag ata	820
109	Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Ile	
110	250 255 260	
111	gaa gat gaa agg aat ctt cat gaa gat ttt gta ttc atg aaa acg ata	868
112	Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr Ile	
113	265 270 275	
114	cag aga tgc aac aca gga gaa aga tcc tta tcc tta ctg aac tgt gag	916
115	Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu	
116	280 285 290 295	
117	gag att aaa agc cag ttt gaa ggc ttt gtg aag gat ata atg tta aac	964
118	Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu Asn	
119	300 305 310	
120	aaa gag gag acg aag aaa gaa aac agc ttt gaa atg caa aaa ggt gat	1012
121	Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly Asp	
122	315 320 325	
123	cag aat cct caa att gcg gca cat gtc ata agt gag gcc agc agt aaa	1060
124	Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys	
125	330 335 340	
126	aca aca tct gtg tta cag tgg gct gaa aaa gga tac tac acc atg agc	1108
127	Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser	
128	345 350 355	
129	aac aac ttg gta acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga	1156
130	Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg	
131	360 365 370 375	
132	caa gga ctc tat tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg	1204
133	Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg	
134	380 385 390	
135	gaa gct tcg agt caa gct cca ttt ata gcc agc ctc tgc cta aag tcc	1252
136	Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser	
137	395 400 405	
138	ccc ggt aga ttc gag aga atc tta ctc aga gct gca aat acc cac agt	1300
139	Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser	
140	410 415 420	
141	tcc gcc aaa cct tgc ggg caa caa tcc att cac ttg gga gga gta ttt	1348
142	Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe	

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144    gaa ttg caa cca ggt gct tcg gtg ttt gtc aat gtg act gat cca agc      1396
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146    440          445          450          455
147    caa gtg agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc      1444
148    Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
149          460          465          470
150    tgaacagtgt caccttgtag gctgtggtgg agctgacgct gggagtcttc ataatacagc      1504
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158 <223> OTHER INFORMATION: Synthetic Construct
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163    20          25          30
164    Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
165    35          40          45
166    Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
167    50          55          60
168    Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
169    65          70          75          80
170    Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
171    85          90          95
172    Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
173    100         105         110
174    Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
175    115         120         125
176    Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
177    130         135         140
178    Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
179    145         150         155         160
180    Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
181    165         170         175
182    Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
183    180         185         190
184    Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
185    195         200         205
186    Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
187    210         215         220
188    Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
189    225         230         235         240
190    Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
191    245         250         255
192    His Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp

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193          260          265          270
194 Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
195          275          280          285
196 Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
197          290          295          300
198 Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
199          305          310          315          320
200 Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
201          325          330          335
202 Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
203          340          345          350
204 Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
205          355          360          365
206 Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
207          370          375          380
208 Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
209          385          390          395          400
210 Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
211          405          410          415
212 Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
213          420          425          430
214 Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
215          435          440          445
216 Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
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218 Ser Phe Gly Leu Leu Lys Leu
219          465          470
221 <210> SEQ ID NO: 3
222 <211> LENGTH: 1574
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Murine surfactant protein D (except CRD) fused to the
227 extracellular domain of murine RANKL/TRANCE
228 <220> FEATURE:
229 <221> NAME/KEY: 5'UTR
230 <222> LOCATION: (7)..(31)
231 <220> FEATURE:
232 <221> NAME/KEY: misc_feature
233 <222> LOCATION: (32)..(799)
234 <223> OTHER INFORMATION: Murine surfactant protein D including hub region,
collagenous
235 portion, and neck, but excluding carbohydrate recognition domain
236 (CRD)
237 <220> FEATURE:
238 <221> NAME/KEY: CDS
239 <222> LOCATION: (32)..(1534)
240 <220> FEATURE:
241 <221> NAME/KEY: sig_peptide
242 <222> LOCATION: (32)..(87)

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Seq#:3; Line(s) 234,246

Seq#:22; Line(s) 785

VERIFICATION SUMMARY

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